DETECTION OF VANCOMYCIN RESISTANT ENTEROCOCCI WITH VAN A GENOTYPE IN CLINICAL ISOLATES FROM A TERTIARYCARE CENTRE

Enterococcal infections may of at least 12 species including *Enterococcus faecalis, E. faecium,E. durans, E. avium, E. casseliflavus, E. gallinarum, E. hirae, E.malodoratus, E. mundtii, E. pseudoavium, E. raffinosus,* and *E. solitarius*. Among enterococcal species, *E.faecalis* and *E. faecium* are the two major human pathogens accounting for 85-89% and 10-15% of all enterococcal infections, respectively. Common to all variants of Vancomycin resistance in enterococci is the ability to cause a change in the structure of the pentapeptide incorporated in the 3 dimensional web of peptidoglycans composing the bacterial cell wall: from the original D-Ala-D-Ala to either D-Ala-D-Lactate (D-Ala-DLac) or D-Ala-D-Serine (D-Ala-D-Ser). *Enterococcus* species have been recognised as a pathogen causing dieases like bacteremia, endocarditis, complicated urinary tract infections, intra abdominal infections, pelvic infections, wound and soft tissue infections etc. VRE has become an important nosocomial pathogen because of its rapid spread, high mortality rates associated with infections, limited option for treatment, and the possibility of transferring vancomycin resistance genes to other more virulent and more prevalent pathogens such as *Staphylococcus aureus.* The VRE isolates study could be harbouring other Van genes. PCR remains the gold standard for diagnosis of Vancomycin resistance. Emerging Vancomycin resistance among Enterococcus is a cause for concern as this leads to a great difficulty in treating serious infections caused by them.

Key words: *E.faecalis,* VRE (vancomycin resistant Enterococci), Van A gene